CRF Errors Corrected by the STIC Systems Branch   **ENTERED**

Serial Number: __09/445,258__

CRF Processing Date: __8/10/2001__
Edited by: _____
Verified by: _____ (STIC sta

#9

- [ ] Changed a file from non-ASCII to ASCII

- [ ] Changed the margins in cases where the sequence text was "wrapped" down to the next line.

- [ ] Edited a format error in the Current Application Data section, specifically: _____

- [ ] Edited the Current Application Data section with the actual current number. The number inputted by the applicant was [ ] the prior application data; or [ ] other _____.

- [ ] Added the mandatory heading and subheadings for "Current Application Data".

- [ ] Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- [ ] Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

- [ ] Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

- [ ] Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

- [ ] Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- [ ] Inserted colons after headings/subheadings. Headings edited included: ·, .

- [ ] Deleted extra, invalid, headings used by an applicant, specifically: _____

- [x] Deleted: [x] non-ASCII "garbage" at the beginning (end of files; [ ] secretary initials/filename at end of file; [ ] page numbers throughout text; [ ] other invalid text, such as_____

- [ ] Inserted mandatory headings, specifically: _____

- [ ] Corrected an obvious error in the response, specifically: _____

- [ ] Edited identifiers where upper case is used but lower case is required, or vice versa.

- [ ] Corrected an error in the Number of Sequences field, specifically: _____

- [ ] A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- [ ] Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a Patentin bug). Sequences corrected: _____

- [ ] Other: _____
_____
_____
_____
_____

·Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

```
                RAW SEQUENCE LISTING              DATE: 08/10/2001
                PATENT APPLICATION:  US/09/445,258    TIME: 08:59:35

                Input Set : A:\Pto.amc
                Output Set: N:\CRF3\08102001\I445258.raw
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 2 <110> APPLICANT: Kato, Seishi
 3         Sekine, Shingo
 4         Kimura, Tomoko
 6 <120> TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE
 7         DOMAINS AND DNAS ENCODING THESE PROTEINS
11 <130> FILE REFERENCE: GIN-6706CPUS
13 <140> CURRENT APPLICATION NUMBER: 09/445,258
14 <141> CURRENT FILING DATE: 1999-12-01
16 <150> PRIOR APPLICATION NUMBER: PCT/US98/02445
17 <151> PRIOR FILING DATE: 1998-06-03
19 <150> PRIOR APPLICATION NUMBER: JP 9-144948
20 <151> PRIOR FILING DATE: 1997-06-03
22 <160> NUMBER OF SEQ ID NOS: 54
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 382
28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
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34 Gly Ala Met Ser Pro Pro Gln Leu Ala Leu Asn Pro Ser Ala Leu Leu
35              20                  25                  30
36 Ser Arg Gly Cys Asn Asp Ser Asp Val Leu Ala Val Ala Gly Phe Ala
37          35                  40                  45
38 Leu Arg Asp Ile Asn Lys Asp Arg Lys Asp Gly Tyr Val Leu Arg Leu
39      50                  55                  60
40 Asn Arg Val Asn Asp Ala Gln Glu Tyr Arg Arg Gly Gly Leu Gly Ser
41 65                  70                  75                  80
42 Leu Phe Tyr Leu Thr Leu Asp Val Leu Glu Thr Asp Cys His Val Leu
43                  85                  90                  95
44 Arg Lys Lys Ala Trp Gln Asp Cys Gly Met Arg Ile Phe Phe Glu Ser
45              100                 105                 110
46 Val Tyr Gly Gln Cys Lys Ala Ile Phe Tyr Met Asn Asn Pro Ser Arg
47          115                 120                 125
48 Val Leu Tyr Leu Ala Ala Tyr Asn Cys Thr Leu Arg Pro Val Ser Lys
49      130                 135                 140
50 Lys Lys Ile Tyr Met Thr Cys Pro Asp Cys Pro Ser Ser Ile Pro Thr
51 145                 150                 155                 160
52 Asp Ser Ser Asn His Gln Val Leu Glu Ala Ala Thr Glu Ser Leu Ala
53                  165                 170                 175
54 Lys Tyr Asn Asn Glu Asn Thr Ser Lys Gln Tyr Ser Leu Phe Lys Val
55                  180                 185                 190
56 Thr Arg Ala Ser Ser Gln Trp Val Val Gly Pro Ser Tyr Phe Val Glu
57              195                 200                 205
58 Tyr Leu Ile Lys Glu Ser Pro Cys Thr Lys Ser Gln Ala Ser Ser Cys
59      210                 215                 220
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60 Ser Leu Gln Ser Ser Asp Ser Val Pro Val Gly Leu Cys Lys Gly Ser
61 225                 230             235                 240
62 Leu Thr Arg Thr His Trp Glu Lys Phe Val Ser Val Thr Cys Asp Phe
63             245             250             255
64 Phe Glu Ser Gln Ala Pro Ala Thr Gly Ser Glu Asn Ser Ala Val Asn
65             260             265             270
66 Gln Lys Pro Thr Asn Leu Pro Lys Val Glu Glu Ser Gln Gln Lys Asn
67         275             280             285
68 Thr Pro Pro Thr Asp Ser Pro Ser Lys Ala Gly Pro Arg Gly Ser Val
69     290             295             300
70 Gln Tyr Leu Pro Asp Leu Asp Asp Lys Asn Ser Gln Glu Lys Gly Pro
71 305             310             315                 320
72 Gln Glu Ala Phe Pro Val His Leu Asp Leu Thr Thr Asn Pro Gln Gly
73             325             330             335
74 Glu Thr Leu Asp Ile Ser Phe Leu Phe Leu Glu Pro Met Glu Glu Lys
75             340             345             350
76 Leu Val Val Leu Pro Phe Pro Lys Glu Lys Ala Arg Thr Ala Glu Cys
77         355             360             365
78 Pro Gly Pro Ala Gln Asn Ala Ser Pro Leu Val Leu Pro Pro
79     370             375             380
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83 <211> LENGTH: 317
84 <212> TYPE: PRT
85 <213> ORGANISM: Homo sapiens
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90 Trp Tyr Arg Glu Arg Gln Val Val Ser His Leu Gln Asp Lys Tyr Val
91             20              25              30
92 Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Leu Ala Arg Gln
93             35              40              45
94 Leu Asp Ala Arg Gly Leu Arg Val Leu Ala Ala Cys Leu Thr Glu Lys
95     50              55              60
96 Gly Ala Glu Gln Leu Arg Gly Gln Thr Ser Asp Arg Leu Glu Thr Val
97 65              70              75                  80
98 Thr Leu Asp Val Thr Lys Met Glu Ser Ile Ala Ala Ala Thr Gln Trp
99             85              90              95
100 Val Lys Glu His Val Gly Asp Arg Gly Leu Trp Gly Leu Val Asn Asn
101             100             105             110
102 Ala Gly Ile Leu Thr Pro Ile Thr Leu Cys Glu Trp Leu Asn Thr Glu
103         115             120             125
104 Asp Ser Met Asn Met Leu Lys Val Asn Leu Ile Gly Val Ile Gln Val
105     130             135             140
106 Thr Leu Ser Met Leu Pro Leu Val Arg Arg Ala Arg Gly Arg Ile Val
107 145             150             155             160
108 Asn Val Ser Ser Ile Leu Gly Arg Val Ala Phe Phe Val Gly Gly Tyr
109             165             170             175
110 Cys Val Ser Lys Tyr Gly Val Glu Ala Phe Ser Asp Ile Leu Arg Arg
111             180             185             190
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112 Glu Ile Gln His Phe Gly Val Lys Ile Ser Ile Val Glu Pro Gly Tyr
113         195                 200                 205
114 Phe Arg Thr Gly Met Thr Asn Met Thr Gln Ser Leu Glu Arg Met Lys
115         210                 215                 220
116 Gln Ser Trp Lys Glu Ala Pro Lys His Ile Lys Glu Thr Tyr Gly Gln
117 225                 230                 235                 240
118 Gln Tyr Phe Asp Ala Leu Tyr Asn Ile Met Lys Glu Gly Leu Leu Asn
119                 245                 250                 255
120 Cys Ser Thr Asn Leu Asn Leu Val Thr Asp Cys Met Glu His Ala Leu
121                 260                 265                 270
122 Thr Ser Val His Pro Arg Thr Arg Tyr Ser Ala Gly Trp Asp Ala Lys
123         275                 280                 285
124 Phe Phe Phe Ile Pro Leu Ser Tyr Leu Pro Thr Ser Leu Ala Asp Tyr
125         290                 295                 300
126 Ile Leu Thr Arg Ser Trp Pro Lys Pro Ala Gln Ala Val
127 305                 310                 315
130 <210> SEQ ID NO: 3
131 <211> LENGTH: 296
132 <212> TYPE: PRT
133 <213> ORGANISM: Homo sapiens
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139         20                  25                  30
140 Leu Ala Gly Val Leu Val Ala Ile Leu Val Gln Val Ser Lys Val Pro
141         35                  40                  45
142 Ser Ser Leu Ser Gln Glu Gln Ser Glu Gln Asp Ala Ile Tyr Gln Asn
143     50                  55                  60
144 Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys
145 65                  70                  75                  80
146 Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly
147                 85                  90                  95
148 Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
149                 100                 105                 110
150 Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln
151         115                 120                 125
152 Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu
153     130                 135                 140
154 Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu
155 145                 150                 155                 160
156 Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile
157                 165                 170                 175
158 Tyr Gln Glu Leu Thr Glu Leu Lys Ala Ala Val Gly Glu Leu Pro Glu
159                 180                 185                 190
160 Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala
161         195                 200                 205
162 Ala Val Gly Glu Leu Pro Asp Gln Ser Lys Gln Gln Gln Ile Tyr Gln
163     210                 215                 220
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164 Glu Leu Thr Asp Leu Lys Thr Ala Phe Glu Arg Leu Cys Arg His Cys
165 225             230             235                 240
166 Pro Lys Asp Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn
167             245             250                 255
168 Ser Gln Arg Asn Trp His Asp Ser Val Thr Ala Cys Gln Glu Val Arg
169             260             265                 270
170 Ala Gln Leu Val Val Ile Lys Thr Ala Glu Glu Gln Leu Pro Ala Val
171         275             280             285
172 Leu Glu Gln Trp Arg Thr Gln Gln
173     290             295
176 <210> SEQ ID NO: 4
177 <211> LENGTH: 197
178 <212> TYPE: PRT
179 <213> ORGANISM: Homo sapiens
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183 1               5               10              15
184 Leu Cys Leu Val Cys Ile Val Ala Asn Ala Leu Leu Leu Val Pro Asn
185             20              25              30
186 Gly Glu Thr Ser Trp Thr Asn Thr Asn His Leu Ser Leu Gln Val Trp
187         35              40              45
188 Leu Met Gly Gly Phe Ile Gly Gly Gly Leu Met Val Leu Cys Pro Gly
189     50              55              60
190 Ile Ala Ala Val Arg Ala Gly Gly Lys Gly Cys Cys Gly Ala Gly Cys
191 65              70              75              80
192 Cys Gly Asn Arg Cys Arg Met Leu Arg Ser Val Phe Ser Ser Ala Phe
193             85              90              95
194 Gly Val Leu Gly Ala Ile Tyr Cys Leu Ser Val Ser Gly Ala Gly Leu
195             100             105             110
196 Arg Asn Gly Pro Arg Cys Leu Met Asn Gly Glu Trp Gly Tyr His Phe
197         115             120             125
198 Glu Asp Thr Ala Gly Ala Tyr Leu Leu Asn Arg Thr Leu Trp Asp Arg
199     130             135             140
200 Cys Glu Ala Pro Pro Arg Val Val Pro Trp Asn Val Thr Leu Phe Ser
201 145             150             155             160
202 Leu Leu Val Ala Ala Ser Cys Leu Glu Ile Val Leu Cys Gly Ile Gln
203             165             170             175
204 Leu Val Asn Ala Thr Ile Gly Val Phe Cys Gly Asp Cys Arg Lys Lys
205         180             185             190
206 Gln Asp Thr Pro His
207         195
210 <210> SEQ ID NO: 5
211 <211> LENGTH: 221
212 <212> TYPE: PRT
213 <213> ORGANISM: Homo sapiens
215 <400> SEQUENCE: 5
216 Met Glu Ala Gly Gly Phe Leu Asp Ser Leu Ile Tyr Gly Ala Cys Val
217 1               5               10              15
218 Val Phe Thr Leu Gly Met Phe Ser Ala Gly Leu Ser Asp Leu Arg His
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219                 20                  25                  30
220  Met Arg Met Thr Arg Ser Val Asp Asn Val Gln Phe Leu Pro Phe Leu
221          35                  40                  45
222  Thr Thr Glu Val Asn Asn Leu Gly Trp Leu Ser Tyr Gly Ala Leu Lys
223      50                  55                  60
224  Gly Asp Gly Ile Leu Ile Val Val Asn Thr Val Gly Ala Ala Leu Gln
225  65                  70                  75                  80
226  Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr Cys Pro Arg Lys Arg Val
227                  85                  90                  95
228  Val Leu Leu Gln Thr Ala Thr Leu Leu Gly Val Leu Leu Leu Gly Tyr
229                  100                 105                 110
230  Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro Glu Ala Arg Leu Gln Gln
231          115                 120                 125
232  Leu Gly Leu Phe Cys Ser Val Phe Thr Ile Ser Met Tyr Leu Ser Pro
233      130                 135                 140
234  Leu Ala Asp Leu Ala Lys Val Ile Gln Thr Lys Ser Thr Gln Cys Leu
235  145                 150                 155                 160
236  Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu Thr Ser Ala Ser Trp Cys
237                  165                 170                 175
238  Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr Ile Met Val Ser Asn Phe
239                  180                 185                 190
240  Pro Gly Ile Val Thr Ser Phe Ile Arg Phe Trp Leu Phe Trp Lys Tyr
241          195                 200                 205
242  Pro Gln Glu Gln Asp Arg Asn Tyr Trp Leu Leu Gln Thr
243      210                 215                 220
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247  <211> LENGTH: 251
248  <212> TYPE: PRT
249  <213> ORGANISM: Homo sapiens
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254  Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly Lys Leu Gly
255                  20                  25                  30
256  Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala Phe Leu Tyr
257          35                  40                  45
258  Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe Tyr Phe Pro Val
259      50                  55                  60
260  Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn Leu Tyr Phe Leu Tyr
261  65                  70                  75                  80
262  Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala Phe Asp Gly Arg Pro Ala
263                  85                  90                  95
264  Asp Tyr Leu Phe Met Leu Leu Phe Asn Trp Ile Cys Ile Val Ile Thr
265                  100                 105                 110
266  Gly Leu Ala Met Asp Met Gln Leu Leu Met Ile Pro Leu Ile Met Ser
267          115                 120                 125
268  Leu Leu Tyr Val Trp Ala Gln Leu Asn Arg Asp Met Ile Val Ser Phe
269          130                 135                 140
270  Trp Phe Gly Thr Arg Phe Lys Ala Cys Tyr Leu Pro Trp Val Ile Leu
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VERIFICATION SUMMARY   DATE: 08/10/2001
PATENT APPLICATION: **US/09/445,258**   TIME: 08:59:36

Input Set : **A:\Pto.amc**
Output Set: **N:\CRF3\08102001\I445258.raw**